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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                               Minimum DB
Maximum DB
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                                                                                                                                  Database
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                                                                                                                                                                                                                               Beq
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A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2003as:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
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length: 2000000000
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version
Copyright (c) 1993 - 2005
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Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Aar25148 Bifunctio	9	Aar25153 Bifunctio	Aar28706 Bifunctio	Aar28704 Bifunctio	Aar28707 Bifunctio	Aar28703 Bifunctio	Aar10110 Trigramin	Aar42867 Platelet	-		Abg30392 Glycoprot	Aab20598 Albolabri		Aaw45500 Albolabri		Aar10106 Trigramin	Aar06395 Albolabri		_	Aae19791 Agkistrod	Aay58231 Korean sn	Aaw14083 Platelet	Aae03036 Agkistrod	Aay79413 Southern	Description	

2 ADF65996 2 AAR280708 2 AAR28708 2 AAR287150 2 AAR25150 2 AAR25150 2 AAR25150 2 AAR25151 2 AAR25151 2 AAR25151 2 AAR25151 2 AAR25151 2 AAR251347 1 AAP31347 1 AAP31347 2 AAR25048 2 AAR25048

ALIGNMENTS

RESULT 1 AAY79413 26-AUG-2004 01-AUG-2000 Southern copperhead snake contortrostatin. AAY79413; AAY79413 standard; protein; 483 (revised)
(first entry) ₽

Southern copperhead snake; venom; contortrostatin; disintegrin; cytostatic; antiproliferative; thrombolyric; cerebroprotective; antiaggregant; antiarteriosclerotic; antianginal; cardiant; metastasis; thrombosis; thromboembolism, stroke; arteriosclerosis; atherosclerosis; embolism; aneurism; angina; myocardial infarction; integrin. Agkistrodon contortrix. Unidentified.

Region Misc-difference Region Key 191. .410
/note= "Metalloproteinase region; a protein comprising
/note region is separately claimed in Claim 3b" /note= "Pro-region; a protein comprising this region is separately claimed in Claim 3c" Location/Qualifiers .190

WO200018421-A1 /note= "Peptide loop, includes RGD sequence at residues 461-463; acts as integrin antagonist"

06-APR-2000.

Region

Peptide

419. 483

/note= "Contortrostatin monomer; a protein this region is separately claimed in Claim 457. 469

comprising

note= "Encoded by CCC"

29-SEP-1999; 98US-00163047. 99WO-US022608

Markland Zhou

(UYSC'-) UNIV SOUTHERN CALIFORNIA.

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RESULT 2
AAE03036
ID AAE0
XX AAE0
AC AAE0
XX AQAI
AX SOUL
KW S
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Best Local
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                                    Region
                                                                                                  Domain
                                                                                                                                                          Binding-site
                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                  Agkistrodon contortrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southern copper head snake; contortrostatin; CN; cytostatic; osteopathic vulnerary; disintegrin; platelet aggregation; neovascularisation; tumour integrin; angiogenesis; metastasis; invasiveness; growth; metastasis; metastasis; carcinoma; carcinoma; sarcoma; therapy; thrombotic disease; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agkistrodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE03036 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Revised record issued
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              embolism, aneurism,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of the Southern copperhead snake venom disintegrin, contortrostatin, a protein that inhibits the interactions between integrins and their receptors. The sequence was deduced from isolated snake venom cDNA (see AAZ94881). The contortrostatin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                         healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DAPANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPR
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                                                                                                                        /label= Metalloproteinase
334. 344
/label= Zinc-binding_moti/
                                                                                                     419.
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                'label= Disintegrin
                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angina and myocardial infarction
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Conserved_sequence
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Pred. No. 1.5e-29;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CN; cytostatic; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to feature table key
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RESULT 3
AAW14083
ID AAW15
AC AAW1
XX
AC AAW1
XX
DT 17-C
DT 27-C
XX
DE Plat
XX
KW Salm
KW Salm
KW Salm
XX
SGloy
XX
PD SGloy
XX
PD SOLO
PO STOLO
PO TO-J
PO TO-J
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is contortrostatin (CN) protein from southern copper head snake. CN, a homodimeric disintegrin binds to integrin alphavbeta5 and induces alphavbeta1. The mediated tyrosine phosphorylation of CAS and FAK in tumour cells. CN is useful for modulating the adhesion, motility, and invasiveness of integrin expressing cells, preferably tumour cells and for inhibiting the adhesion of integrin expressing cells to vitronectin. The pharmaceutical composition comprising CN is useful for inhibiting platelet aggregation, neovascularisation, angiogenesis, tumour metastasis, invasiveness or growth, for inhibiting metastasis, invasiveness or growth, for inhibiting metastasis in malanoma, carcinoma and sarcoma patients. It is also useful for treating thrombotic diseases, osteoporosis, and wound healing in mammals
                                                                         Gloydius halys brevicaudus
                                                                                                     Salmosin; inhibit; blood; platelet aggregation; venom; K
salmosa viper; Agkistrodon halys brevicaudus; treatment;
                                                                                                                                                 Platelet aggregation inhibitor,
                                                                                                                                                                               17-OCT-2003
27-OCT-1997
                                                                                                                                                                                                                            AAW14083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 12; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAD07386.
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08-JUN-2000;
                                             FR2736266-A1
                                                                                                                                                                                                                                                        AAW14083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invasiveness of integrin expressing tumor cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYSC-) UNIV SOUTHERN CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483
                                                                                                                                                                                                                                                                                                                                                                                            DAPANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPR
                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                  NPFHA 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; illarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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2000US-00591552.
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                                                                                                                                                                             (revised)
(first entry)
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PCR-1 and PCR-2"
461. _463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101pp;
                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGD_sequence
                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 382; DB 4;
Pred. No. 1.5e-29;
; Mismatches 0;
                                                                                                                                                   Salmosin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 483;
                                                                                                                       Korean
                                                                                                        thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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RESULT 4
AAYS231
ID SAZS
XX AAYS
XX AAYS
XX AAYS
DT 12-S
DT 27-M
XX Kore
XX Salu
Meta
XX Salu
KY Rey
FT Regi
FT Regi
FT Regi
FT Regi
XX XX Salu
XX Meta
XX Met
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Best Local S
Matches 56
  WPI; 2000-064611/06.
N-PSDB; AAZ55609.
                                                                    Kim D,
                                                                                                                                                              23-JUN-1998;
04-JUN-1999;
                                                                                                                                                                                                                                                                                                                              EP967276-A2
                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salmosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This peptide, designated Salmosin, inhibits blood platelet aggregation. It is derived from the venom. of the Korean salmosa viger 'Agkistroden halys brevicaudus). Salmosin can be used, in particular, in compositions for management of thrombosis. Salmosin also has higher activity than kistrin, gamma-trigramin and echistatin. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide derived from Korean salmosa viper venom - useful as blood platelet aggregation inhibitor, for the management of thrombosis.
                                                                                                                                                                                                                                  23-JUN-1999;
                                                                                                                                                                                                                                                                             29-DEC-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis;
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27-MAR-2000
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standardise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 11; 15pp; Frénch.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gloydius halys.
                                                                                                               (KIMD/) KIM D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Korean anake venom salmosin.
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                                                                 Chung KH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDYCNGISAGCPRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma-trigramin
ise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     angiogenesis; inhibitor; integrin; antagonist; disintegrin;
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A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
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(first entry)
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                                                                                                                                                              98KR-00023778
99KR-00020579
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tumour.
                                                                                                                                                                                                                                                                                                                                                                       "RGD motif"
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Pred. No. 9.4e-27;
5; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INST.
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RESULT 5
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the former being a marker of angiogenic blood vessels and certain malignant cells. Disintegrins inhibit tumour metastasis by blocking tumour cell adhesion to the extracellular matrix, and antagonism of integrin alpha-v-beta-3 can suppress tumour-induced angiogenesis. Salmosin can be used as an anticancer agent. It may be used for the inhibition or reduction of tumour cell angiogenesis, the inhibition of metastatic tumour formation and the inhibition or reduction of metastatic tumour growth. Nucleotides encoding salmosin may be used in gene therapy applications. Many types of cancer may be tracted with salmosin or nucleotides encoding it, including leukaemia and cancers of the breast, ovary, uterus, skin, lung, larynx, colon, pancreas, testis, liver, brain, muscle and bone. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                         Hong
                                                                                                                                                                                                                                                                                                   Gloydius halys brevicaudus.
                                                                                                                                                                                                                                                                                                                               Korean snake; saxatilin; anticoagulant; cytostatic; venom; anti-tumour; platelet aggregation; angiogenesis; salmosin; cytotoxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of small proteins mainly derived from snake venom which contain an RGD or KGD motif (the structural motif recognised by platelet fibrinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a 7.5 kD salmosin protein of a Korean snake, Agkistrodon halys brevicaudus. Salmosin is a disintegrin, a family of small proteins mainly derived from snake venom which contain an RGD o
         New cDNA encoding Saxatilin protein derived from venom of Korean snake
Agkistrodon saxatilis emelianov, useful as anti-platelet aggregation
                                                                                                                                                                                                       26-JUL-2000; 2000WO-KR000809
                                                                                                                                                                                                                                       21-FEB-2002.
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18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAE19791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor alpha-2-b-beta-3). Disintegrins act as potent antagonists of several integrins including alpha-v-beta-3 and alpha-5-beta-1 integrins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel
                                                           WPI; 2002-241903/29.
                                                                                                                                                                      26-JUL-2000; 2000WO-KR000809
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                                                                                                                                                                                                                                                                                                                                                                               Agkistrodon halys brevicaudus salmosin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE19791 standard;
                                                                                                                         (CHUN/) CHUNG K. (KIMD/) KIM D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides used for antitumor therapy
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                                                                                         Koh Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFHA
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(first en
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                                                                                         Sohn
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Pred. No. 9
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.4e-27;
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agent and anti-tumor agent.

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Best Local S
Matches 56
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07-AUG-2003
18-JUN-2002
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                                                                                                                                          Hong
                                                                                                                                                               (CHUN/)
The invention relates to a cDNA encoding Saxatilin protein derived from venom of Korean snake Agkistrodon saxatilis emelianov. The cDNA is usefi for as an anti-tumour agent and for effectively suppressing platelet
                                             Claim
                                                               New cDNA encoding Saxatilin protein derived Agkistrodon saxatilis emelianov, useful as agent and anti-tumor agent.
                                                                                                            N-PSDB;
                                                                                                                                                                                                26-JUL-2000; 2000WO-KR000809
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                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                             Gloydius halys
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                                                                                                                                                                                                                                                                                                                                                                                Agkistrodon
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                                                                                                          2002-241903/29.
DB; AAD31060.
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                                                                                                                                                               CHUNG
KIM D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDYCNGISAGCPRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                          Koh Y,
                                                                                                                                                                                                                                                                                                                                               aggregation; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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(revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                           saxatilin; anticoagulant; cytostatic;
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                                          35; 41pp; English
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                   /note= "Encoded by GGA"
                                                                                                                                           Sohn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.6%;
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                                                                                                                                          You
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Pred. No. 9.4e-27;
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                                                                                                                                                                                                                                                                                                                                                                                saxatilin protein.
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                                                                                                                                          Jang
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                                                                                                                                           Huh
                                                                          d from venom of Korean snake anti-platelet aggregation
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                                                                                                                                                                                                                                                                                                                                                             venom; anti-tumour;
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            is useful
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Best Local S
Matches 56
        The sequence is deduced from the coding strand of a synthetic gene for a polypeptide inhibitor of platelet activation. The polypeptide is analogous to that obtd. from the venom of Agkistrodon p. piscivorus (North American Water Moccasin). The gene can be used to produce recombinant inhibitor or fusion proteins with eg. hirudin derivs. These can be used to decrease/ inhibit platelet aggregation and release in viv. or in vitro. Usual dose is 0.01-100 mg/kg body wt. The recombinant protein can also be used to coat the surfaces of invasive medical devices. It can also block stenosis and spassm at the site of thrombosis by inhibiting the release of thromboxan A2 ). See also AAR06508. (Updates on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                   27-JAN-1989;
27-JAN-1989;
01-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aggregation which makes it possible as and an active ingredient of antipatelet agent. Saxatilin is useful for inhibiting angiogenesis induced by tumour and for inhibiting tumour without cytotoxicity. The present sequence is Agkistrodon saxatilis emelianov saxatilin protein. (Updated on 07-AUG-2003 to correct OS field.) (Updated on 29-AUG-2003 to
                                                                                                                                                                                                                                                          WPI; 1990-260891/34.
N-PSDB; AAQ05730.
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04-JAN-1991
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                                                                                                                                                                         Claim 3; Fig 9; 73pp; English
                                                                                                                                                                                                     for preventing agglutination recombinant dna encoding it.
                                                                                                                                                                                                                   Pure platelet activation inhibiting polypeptide from snake venom for preventing agglutination and release in vivo or vitro, and no
                                                                                                                                                                                                                                                                                                  Maraganore J,
                                                                                                                                                                                                                                                                                                                           (UYBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                        27-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                09-AUG-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9008772-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Snake venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Platelet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR06494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR06494 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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                                                                                                                                                                                                                                                                                                                            UNIV BOSTON.
BIOGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aggregation inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thromboxan A2; thrombosis; anti-coagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
(first entry)
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89US-00303590.
89US-00430313.
                                                                                                                                                                                                                                                                                                  Jakubowski
                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00303585
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87.5%;
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Pred. No. 1.2e-26;
5; Mismatches 3;
                                                                                                                                                                                                                                                                                                     Chao
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RESULT 8
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                                                                                    Query Match
Best Local S
Matches 54
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Best Local
                                                                                                                                                                                                                                                               The peptide is prepd. from the venom of the viper T. albolabris or may be prepd. by genetic engineering or solid phase synthesis. It inhibits both fibrin binding to human platelets and fibrinogen- induced aggregation of human platelets. It is eliminated from the ciculation rapidly and is therefore useful in situations where a strong antithrombic action of
                                                                                                                                                            Sequence
                                                                                                                                                                                                           short duration is neede, e.g. in surgery on peripheral arteries, cardiovascular surgery and the interaction of platelets with artisurfaces. See also AAR06389-97. (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Page 13; 13pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            Viper venom polypeptide(s) - useful for inhibiting fibrinogen binding human platelets and inhibiting fibrinogen-induced aggregation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Niewiarows S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Friedman PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI )
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13-DEC-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fibrinogen binding; inhibitor; platelet aggregation; thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FRIE/)
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UNIV TEMPLE.
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRIEDMAN P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                            73
                SPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRN
                                       APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs JW,
Holt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            first entry)
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                                                                                                     87.4%;
84.4%;
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Rucinski B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gould
                                                                                Score 334; DB 2; 1
Pred. No. 1.4e-25;
5; Mismatches 5;
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
.2e-26;
                                                                                                                    Length 73;
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RESULT 10
AAR53946
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AAR10106
ID AAR1
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Best Local :
                                                          27-AUG-2003
25-MAR-2003
21-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence was produced by recombinant techniques using a synthetic gene prepd. from 10 oligonuclectides based on the amino acid sequence determined by Edman degardation. The recombinant trigramin-gamma is used in treatment of hypercoagulation-related states. See also AAR10107-R10113
Disintegrin; Viperidae; snake; integrin; inhibitor; fibrinogen;
                             Disintegrin
                                                                                                                          AAR53946;
                                                                                                                                                        AAR53946 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Platelet aggregation inhibiting amino acid sequences - are derived from snake venom and inhibit fibrinogen binding to GP IIA-GP IIIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Platelet aggregation inhibitor; snake venom; fibrin binding; inhibition; GP IIA; GP IIIA; hypercoagulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 1; 91pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lazarus R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                2 APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                             peptide #14
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                          (revised)
(revised)
(first entry)
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                                                                                                                                                        peptide;
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                                                                                                                                                                                                                                                                                                                                                                             87.4%;
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                                                                                                                                                                                                                                                                                                                                                                             Score 334; DB 2;
Pred. No. 1.4e-25;
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RESULT 11
AAW45500
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequences given in AAR53933-46 are disintegrin peptides. Disintegrins are low molecular weight proceans from the Vaperidae family of snakes which bind integrin proteins similar to the endogenous messenger and structurally interactive molecules. Disintegrins are competitive inhibitors of biomolecules, such as fibrinogen, for integrin binding sites such as GP IIb/IIIa on human platelets. Disintegrins contain the tripeptide sequence Arg-Gly-Asp. Radiolabelled disintegrin peptides can be used for the treatment and diagnosis of venous and arterial thrombis pulmonary emboli and tumours or abscesses that have a thrombus component. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
06-JUN-1996;
                         19-DEC-1996.
                                                                                                        glycoprotein
                                                                                                                       Contrast agent; targeted composition; diagnosis; diseased tissue;
                                                                                                                                               Albolabrin peptide targeting ligand
                                                                                                                                                                             20-MAY-1998
                                                                                                                                                                                                                                 AAW45500 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; Page 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Radio-labelled polypeptide(s) derived from Viperidae disintegrin(s) - for treatment and diagnosis of venous and arterial thrombi, pulmonary emboli and tumours or abscesses having a thrombus component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-151248/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Knight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trimeresurus albolabris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrin binding sites; GP IIb/IIIa; human; platelets; radiolabel; treatment; diagnosis; venous; arterial; thrombi; pulmonary emboli;
                                                     WO9640285-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abscesses; thrombus component.
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                                                                                                                                                                            (first entry)
                                                                                                        GPIIb/IIIa receptor; albolabrin.
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96WO-US009938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62pp; English.
                                                                                                                                                                                                                                 peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 334; DB 2;
Pred. No. 1.4e-25;
5; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
                                                                               bioactive agent; anionic lipid; cationic counter ion; lipid covalently bonded to a polymer; ultrasound; charged lipid; targeted drug delivery; diagnostic imaging; targeting ligand; GPIIbIIIa receptor; diagnosis; vascular thrombosis; clot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contrast agent or targeted compsn. for imaging or treating diseased tissue - comprising lipid, protein or polymer, a gas, and a targetin ligand e.g. a protein, peptide, saccharide or steroid.
                                                 Unidentified
                                                                                                                                                                         Composition targeting ligand peptide Albolabrin.
                                                                                                                                                                                                            25-MAR-2004
                                                                                                                                                                                                                                                                                ADH67966 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 57; 175pp; English.
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01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a targeting ligand. The invention relates
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96US-00640464.
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Pred. No. 1.4e-25;
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KW myoca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a method of: (A) delivering a bioactive agent (BA) to a patient by: (a) administering a composition comprising: (i) an anionic lipid (AL); (ii) a cantionic counter ion (CCI); (iii) a lipid C cavalently bonded to a polymer (LbP), and (iv) BA, and (b) applying therapeutic ultrasound to facilitate delivery of BA in a desired region; (B) delivering a BA to a patient, comprising administering a composition comprising a charged lipid (CL), a counter ion (CI), LbP, BA and the patient, comprising composition of a patient, comprising: (a) administering a composition comprising CL, CI and LbP of the composition in (B), and (b) scanning the patient using Cd diagnostic imaging, to give visible images of the region, and (D) contrast agent composition in (B), and (b) scanning the patient using components as in (Ca). The compositions processes described above may be used in drug delivery, targeted drug delivery, therapeutic imaging and diagnostic imaging. This sequence represents an example of a targeting ligand designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local (
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06-MAY-1997;
18-JUN-1997;
02-JUL-1997;
08-SEP-1997;
                                                                                Targeting ligand peptide; imaging; ultrasound; vesicle; tumour; myocardial; endothelial; epithelial; glycoprotein GPIIbIIIa receptor; detection; thrombus; integrin; malignancy; inflammation; lesion; atherosclerotic plaque; carcinoma.
                 WO200045856-A2
                                                  Unidentified
                                                                                                                                                                                                   12-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Processes for drug delivery, therapeutic comprises use of compositions comprising lipid covalently bonded to polymer.
                                                                                                                                                                  Albolabrin targeting ligand peptide.
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                                                                                                                                                                                                                                                                AAB20598 standard; peptide; 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                         54;
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                                                                                                                                                                                                 (first entry)
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97US-00851780.
97US-00877826.
97US-00887215.
97US-00925353.
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Pred. No. 1.4e-25
5; Mismatches
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RESULT 14
ABG30392
ID ABG30
XX Targe
KW Targe
KW Glycc
XX Unide
XX Unide
XX Unide
XX Unide
XX 10-M
XX 10-M
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XX 30-OC
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XX (1MA)
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Best Local S
Matches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes an ultrasound method comprising: (i) administering a targeted vesicle composition (A); and (ii) scanning the subject by exposure to a first type of ultrasound energy and then interrogating with a second type of ultrasound energy. (A) consists of a vesicle comprising a lipid, protein or polymer, encapsulating a gas, in combination with a targeting ligand. The method is used to detect: (I) a thrombus (particularly old or echogenic); (II) a low concentration of vesicles; or (III) vesicles targeted to endothelial tissue, particularly those containing integrins associated with malignancy or inflammation in early or small lesions, e.g. atherosclerotic plaque or ovarian, endometrial or other carcinomas. The method increases the signal from microbubbles and reduces background noise. The present sequence represents a targeting ligand peptide which is used in the method of the present argeting ligand peptide which is used in the method of the
                                                                                                                                                                                                                    Target vesicle; diagnostic imaging; thrombus; cancer; albolabrin; arteriosclerosis; atherosclerotic plaque; infarcted myocardium; glycoprotein GPIIbIIIa receptor; targeting ligand.
                                                                                                                                                                                                                                                                                      Glycoprotein GpIIbIIIa targeting ligand Albolabrin.
                                                                                                                                                                                                                                                                                                                           07-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73
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                                                                                   17-OCT-2001;
                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention
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                   (IMAR-) IMARX THERAPEUTICS INC
                                                 30-OCT-2000; 2000US-00699679.
                                                                                                                     10-MAY-2002
                                                                                                                                                      WO200236161-A2
                                                                                                                                                                                                                                                                                                                                                                                           ABG30392 standard; protein; 73
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Pred. No. 1.4e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel targeted compound having a combination of hydrophobic compound, hydrophilic polymer and targeting ligand. The invention also comprises a target vesicle composition comprising lipid, protain or polymer gas filled vesicles in an aqueous carrier, a method for imaging a thrombus in a region of a patient involving administering to the patient a target vehicle composition and scanning the region (preferably cardiac region) with diagnostic maging (preferably diagnostic ultrasound) and a method for lysing a thrombus in a blood vessel. The invention also comprises a method for providing an image of an internal region of a patient which can be used to obtain a visible
03-FEB-1999;
                                                                                                                                                gastrointestinal
                                                                                                                                                                Ultrasound method; targeted vesicle composition; targeting ligand; ultrasound scanning; dual frequency ultrasound insonation; micelle; liposome; phospholipid; ultrasound energy; vesicle oscillation; reflected ultrasound signal; ultrasound diagnosis; echogenic thrombus; endothelial tissue; epithelial cell; tumour cell; myocardial cell; integrin; malignancy; inflammation; heart; diseased tissue; imaging;
                                                                                                                                                                                                                                                                                                 Targeting
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                                     18-FEB-2003
                                                                        US6521211-B1
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                                                                                                                                                                                                                                                                                                                                                                              ABU63163;
                                                                                                                                                                                                                                                                                                                                                                                                                   ABU63163 standard;
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                                                                                                                                                                                                                                                                                                   ligand #13 used in novel diagnostic ultrasound
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99US-00243640
                                                                                                                                                region;
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84.4%;
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Search completed: November Job time : 75 secs

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08:15:50

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PLHA

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                                                                                                                                                                                                                                                                                                                                                                                palmitry/glyverophosphoethanolamine and phosphatidic acids. The method of scanning involves exposing the patient to a first ultrasound energy having a first insonation frequency to cause the vesicle to oscillate, and then subsequently, while the vesicle is oscillating, exposing the patient to a second ultrasound energy having a second insonation frequency that is different from the first insonation frequency, and detecting the reflected ultrasound signal. The method is useful for ultrasound diagnosis, for detection of a thrombus or enhancement of thrombus (e.g. old or echogenic thrombus) and for detecting vesicles targeted to epithelial cells, tumour cells, myocardial cells, and cendothelial tissue including integrins associated with malignancy or inflammation. The method is also useful for diagnosing the presence or absence of diseased tissue in a patient, and for imaging one or more regions of a patient, such as for providing images of the heart, gastrointestinal region or lymphatic systems. ABU63151-ABU63172 represent targeting ligands that may be used in the method of the present invention
                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a novel ultrasound method which involves administering to a patient a targeted vesicle composition which comprises vesicles encapsulating agas, in combination with a targeting ligand, and scanning the patient using dual frequency ultrasound insonation. The vesicles themselves comprise a lipid, protein or polymer, and are selected from liposomes and micelles. The vesicles may comprise a phospholipid selected from diolecylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, distearcylphosphatidylcholine, dipalmitoylphosphatidylcholine, dipalmitoylphosphatidylcholine, diolecylphosphatidylcholine, dipalmitoylphosphatidylcholine, diolecylphosphatidylcholine, dipalmitoylphosphatidylcholine, diolecylphosphatidylethanolamine, l-hexadecyl-2-spicinyldiolecylphosphatidylethanolamine, l-hexadecyl-2-spiciny
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01-MAY-1996;
06-JUN-1996;
06-FEB-1998;
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                                                                                                                                                                                                                                                                                                                              Sequence 73
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                                                                                                                            2 APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
                                                                                                                                                                                                                                Similarity
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96US-00640464.
96US-00660032.
98US-0073913P.
98US-00218660.
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Pred. No. 1.4e-25;
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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  Score
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seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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382
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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  GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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45	44	43	42	41	40	39	38	37	36	ω 5	34	33	32	31	30
188.5	189	191	192.5	194	194.5	195.5	195.5	196.5	199	214	221.5	223.5	228	235	236
49.3	49.5	50.0	50.4	50.8	50.9	51.2	51.2	51.4	52.1	56.0	58.0	58.5	59.7	61.5	61.8
419	50	49	610	47	419	609	571	617	429	616	83	83	478	478	478
N	N	N	N	N	N	N	N	N	N	N	Ν	N	N	N	N
S41607	S53431	A32029	JC7530	A35982	A59414	855270	S24789	S48160	A42972	A55796	A34156	F35982	A43296	JC4880	JQ1301
atrolysin A (EC 3.	echistatin beta -	echistatin alpha-1	vascular apoptosis	echistatin alpha-2	metalloproteinase	catrocollastatin p	jararhagin C precu	metalloproteinase	coagulation factor	ecarin precursor -	bitistatin - puff	bitan alpha - puff	atrolysin E (EC 3.	fibrinolytic metal	hemorrhagic protei

ALIGNMENTS

RESULT 2 JC8020 JC8020 metalloproteinase-disintegrin protein, Jerdonitin - Trimeresurus jerdonii C;Species: Trimeresurus jerdonii C;Date: 04-Apr-2004 #sequence revision 04-Apr-2004 #text_change 04-Apr-2004 C;Accession: JC8020; PC7231 R;Chen, R.Q.; Jin, Y.; Wu, J.B.; Zhou, X.D.; Lu, Q.M.; Wang, W.Y.; Xiong, Y.L. Biochem. Biophys. Res. Commun. 310, 182-187, 2003 A;Title: A new protein structure of P-II class snake venom metalloproteinases: It compri A;Reference number: JC8020; PMID: 14511668 A;Accession: JC8020 A;Molecule type: mRNA A;Residues: 1-484 <che> A;Cross-references: GB:AY364231 A;Reperimental source: Crude venom A;Accession: PC7231 A;Molecule type: protein A;Accession: PC7231 A;Molecule type: protein A;Residues: 206-214;221-233;29-308;310-344;451-453;460-484 <ch2> C;Comment: This protein, a new metalloproteinase-disintegrin protein, belongs to the classin with IC50 of 120nM. C;Keywords: Jerdonitin; metalloproteinase-disintegrin; platelet aggregation; SVMP</ch2></che>	QUELY MALCH STORY BEST LOCAL Similarity 87.5%; SCOLE 346; DB 2; DELIGHT 1; Best Local Similarity 87.5%; Pred. No. 3.2e-27; Matches 56; Conservative 5; Mismatches 3; Indels 0; Gaps 0; Qy 2 APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61	egation disintegrin (brevicaudin) 2b, veydius halys brevicaudus -2002 #sequence_revision 01-Mar-2002 #t 459409 Sci. Reports 30, 71-78, 2000 stion and Primary Structures of Platelet imber: A59409 1.859409 1.859409 1.819107 1.4TER- 2011 2011 2011 2011 2011 2011 2011 201

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Proc. Natl. Acad. Sci. U.S.A. 87, 2471-2475, 1990
A;Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: 6
A;Reference number: A35982; MUID:90207217; PMID:2320569
A;Status. Procession: E35982
                                                                                                                                                                                                                                                RESULT 4
E35982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: venom
F;1-69/Domain: disintegrin homology (fragment) <DIS>F;51-53/Region: cell attachment (R-G-D) motif
F;29-59,47-66/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Jaseja, M.; Smith, K.J.; Lu, X.; Williams, J.A.; Trayer, H.; Trayer, I.P.; Hyde, E.I. Eur. J. Biochem. 218, 853-860, 1993
A;Title: (1)H-NMR studies and secondary structure of the RGD-containing snake toxin, alk A;Reference number: S43021; MUID:94109384; PMID:8281937
A;Accession: S43021
A;Status: preliminary
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A;Cross-references: UNIPROCC;Superfamily: disintegrin
                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-73 <DEN>
                                                                                                                                                                       trigramin gamma - Indian green tree viper
C;Species: Trimerseurus gramineus (Indian green tree viper)
C;Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change
C;Accession: E35982
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              UNIPROT: P17496
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84.4%;
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Pred. No. 4.8e-26;
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Pred. No. 1.2e-25;
4; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>υ</u>
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                62
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platelet-aggregation disintegrin (brevicaudin) la - Gloydius halys brevicaudus
C;Species: Gloydius halys brevicaudus
C;Dete: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 09-Jul-2004
C;Accession: A59411
R;Terada, S.
Fukuoka Univ. Sci. Reports 30, 71-78, 2000
A;Title: Isolation and Primary Structures of Platelet Aggregation Inhibitors from Gloydi
A;Reference number: A59409
A;Accession: A59411
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-71 - TER's
A;Cross-references: UNIPROT:090220
C;Keywords: anticoagulant; integrin inhibitor; venom
                                                                                                                                                                                                                                                                                                           platelet aggregation disintegrin (brevicaudin) C;Species: Gloydius halys brevicaudus C;Date: 01-Mar-2002 #sequence_revision 01-Mar-2C;Accession: A59410
                                                                                                                                    A;Cross-references: UNIPROT:Q90220 C;Keywords: anticoagulant; integrin inhibitor; venom
                                                                                                                                                                          A; Molecule type: protein A; Residues: 1-73 < TER>
                                                                                                                                                                                                                          A; Reference number: A; Accession: A59410
                                                                                                                                                                                                                                                             Fukuoka Univ. Sci. Reports 30, A; Title: Isolation and Primary
                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                           Fukuoka Univ. Sci.
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nilarity 84.4%;
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Pred. No. 6e-2
6; Mismatches
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Pred. No. 5.9e-26;
6; Mismatches 4
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A;Title: Trigramin: primary structure and its inhibition of A;Reference number: A30065; MUID:89229063; PMID:2653425
A;Accession: A30065
A;Molecule type: protein
A;Residues: 408-479 <HUA>
A;Residues: 408-479 <HUA>
R;Huang, T.F.; Holt, J.C.; Lukasiewicz, H.; Niewiarowski, S.
J. Biol. Chem. 262; 16157-16163, 1987
A;Title: Trigramin. A low molecular weight peptide inhibiting A;Resession: A29784; MUID:88058981; PMID:3680247
A;Accession: A29784
A;Molecule type: protein
A;Residues: 408-419 <HUZ>
C;Superfamily: trigramin precursor; disintegrin homology
C;Keywords: anticoagulant; glycoprotein; hydrolase; metallop:
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A;Title: Platelet glycoprotein IIb-IIIa protein antagonists from snake venoms: evidence A;Reference number: A35982; MUID:90207217; PMID:2320569
A;Accession: D35982
                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT: P15503; EMBL:X51530; NID:g64407; PIDN:CAA35910.1; A;NOte: translation of the signal sequence and the mature protein but not of tR;Huang, T.F.; Holt, J.C.; Kirby, E.P.; Niewiarowski, S. Biochemistry 28, 661-666, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids Res. 18, 4255, 1990
A;Title: Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin A;Reference number: S12589; MUID:90332429; PMID:2377470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trigramin precursor - Indian green tree viper N;Concains: hemorrhagic proceinase (EC 3.4.4.); platelet aggregation inhibitor C;Species: Trimeresurus gramineus (Indian green tree viper) C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004 C;Accession: S12589; A30065; A29784
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A30065
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Nucleic Acids Res.
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A; Accession: C35982
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precursor; disintegrin homology
c; glycoprotein; hydrolase; metalloproteinase; venom; zinc;
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Pred. No. 2.9e-25;
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A;Cross-references: UNIPROT:P31987
C;Superfamily: disintegrin homology
F;2-68/Domain: disintegrin
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J. Biol. Chem. 268, 1058-1065, 19
A;Title: Characterization of the
                                                                                                                                                                                                                                                                                                        platelet aggregation disintegrin (viridin), venom - prairie rattlesnake C;Species: Crotalus viridis viridis (prairie rattlesnake) C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-C;Accession: G43019
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A;Title: Agkistrodon piscivorus piscivorus platelet aggregation inhibitor: a A;Reference number: A33990; MUID:90046735; PMID:2510158
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                                                                                                                                          A; Molecule type: protein A; Residues: 1-71 <SCA>
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C;Date: 23-Mar_1990 #sequence_revision 23-Mar-1990 #text_change 09
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47; Conser
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                                                                       disintegrin homology disintegrin homology <DIS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480
                                                                                                                                                                                                                          A43019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.2%;
85.7%;
                   74.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84.3%;
                                                                                                                                                                                                                            f the integrin specificities MUID:93123215; PMID:8419314
                                                                                                                                                                                                                                                                                    Naughton, M.A.; Phillips,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ა</u>
Score 286; DB 2;
Pred. No. 2.3e-21;
7; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 322; DB 1;
Pred. No. 2.8e-24;
5; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 321.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8e-25;
nes 3;
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                                  Length 71;
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                                                                                                                                                                                                                                                                                    D.R.; Nannizzi, L.; Arfsten,
                                                                                                                                                                                                                                                disintegrins
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inh Mar

Conservative

7;

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Gaps

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A;Cross-references: UNIPROT:P31981
C;Superfamily: disintegrin horal
F;2-68/Domai-
                                                                                                                                                                                                                                                                                                                                                                                                      platelet aggregation disintegrin (molossin), venom - Northern blacktail rattlesnake C;Species: Crotalus molossus molossus (Northern blacktail rattlesnake) C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004 C;Accession: H43019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, J. Biol. Chem. 268, 1058-1065, 1938
A;Title: Characterization of the integrin specificities of disintegrins is A;Reference number: A43019; MUID:93123215; PMID:8419314
A;Accession: 143019
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                                                                                                                                                                                                                                                                                                                                                                         R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; J. Biol. Chem. 268, 1058-1065, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platelet aggregation disintegrin (basilicin), venom - Mexican West-Coast rattlesnake C;Species: Crotalus basiliscus basiliscus (Mexican West-Coast rattlesnake) C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004 C;Accession: I43019
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RESULT 13
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                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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Best Local S
Matches 47
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Best Local 9
                                                                                                                                                                                                                                             Superfamily:
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                                                                                                                                                                  47;
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                                                                                                                                                                                                                                disintegrin homology <DIS>
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73.4%;
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Pred. No. 2.3e-21;
8; Mismatches 9
                                                                                                                                                                                    Score 285; DB 2;
Pred. No. 2.9e-21;
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                                                                                                                                                                     Mismatches
                                                                                                                                                                     10;
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RESULT 15 B40003

Ś 밁 5

platelet aggregation disintegrin (tergeminin), venom - western massasauga (;Species: Sistrurus catenatus tergeminus (western massasauga) C;Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-200 C;Accession: B40003 Rose, J.W.; Hsu, M.A.; Phillips, D.R.; Fried, V.A.; (R.;Carborough, R.M.; Rose, J.W.; Hsu, M.A.; Phillips, D.R.; Fried, V.A.; (J. Biol. Chem. 266, 9359-9362, 1991 A;Title: Barbourin. A GPIIb-IIIa-specific integrin antagonist from the ven A;Reference number: A40003; MUID:91236695; PMID:2033037 A;Status: preliminary

V.A.; Campbell,

Α.Μ

venom of Sistruru

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platelet aggregation disintegrin (lachesin), venom - bushmaster C;Species: Lachesis muta (bushmaster) C;Species: Lachesis muta (bushmaster) C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 16-Aug-2004 C;Accession: E43019
C;Accession: E43019
C;Accession: Majoria Majoria Mushton, M.A.; Phillips, D.R.; Nannizzi, R;Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, J. Biol. Chem. 268, 1058-1065, 1993
A,Title: Characterization of the integrin specificities of disintegrins iso A,Reference number: A43019; MUID:93123215; PMID:8419314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R.Scarborough, R.M.; Rose, J.W.; Naughton, M.A.; Phillips, D.R.; Nannizzi, L.; Arfsten, J. Biol. Chem. 268, 1058-1065, 1993
A;Title: Characterization of the integrin specificities of disintegrins isolated from A A;Reference number: A43019; MUID:93123215; PMID:8419314
A;Accession: B43020
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-72 <SCA>
                                                                                                                                                                                                                                                                                     A;Accession: E43019
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-73 <SCA>
A;Cross-references: UNIPROT:P31990
C;Superfamily: disintegrin homology
F;3-69/Domain: disintegrin homology <DIS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P31985
C;Superfamily: unassigned disintegrins; disintegrin homology
F;3-69/Domain: disintegrin homology <DIS>
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70
                                             62 PFH 64
                                                                                             10 APANPCCDAATCKLRPGAQCAEGLCCDQCRFIKKGKICRRARGDNPDDRCTGQSADCPRN
                                                                                                                                                                                          45;
                                                                                                                      2 APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
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GYY 72
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73.0%;
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Pred. No. 2.
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Pred. No. 5.7e-21;
8; Mismatches 9
                                                                                                                                                                                               Mismatches
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.2e-20;
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A.Residues: 173.6CA>
A.CROSG-references: NUTRROT: P22828
A.CROSG-references: NUTRROT: P22828
F.3-69/Domain: disintegrin homology cD15>

Query Match | Similarity | 71.2%; Score 272; DB 2; Length 73;
Best Local Similarity | 73.3%; Pred. No. 5.4e-20;
Matches 47; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
Matches 47: Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 2 APANPCCDANTCKLTGSQCLDGLCCDQCKFMXEGTVCRAAKGDMXDDTCTQSACCPRW 61
10 SPANPCCDANTCKLEPGACADSLCCDQCKFMXEGTVCRAAKGDMXDDTCTQSACCPRW 65
Search completed: November 3, 2005, 08:19:35
Job time: 40 secs
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length: 2000000000
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Match Length
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382
1 DAPANPCCDAATCKLTTGSQ......DLDDYCNGISAGCPRNPFHA
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1: uniprot_sprot:*
2: uniprot_trembl:*
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen
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188.052 Million cell updates/sec
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i through a collaboration ind the EMBL outstation—no restrictions on its content is in no way by and for commercial (www.isb-sib.ch/announce/	(EC 3.4.24) irhead). a; Euteleostomi; Colubroidea; colubroidea; , COPACTOR, AND a subunit of dimeric a subunit of dimeric evenom zinc protease action with platelet complex. Acts by on the platelet pregation in human milarity). ha and a beta and.	Q7sze0 gloydius sa p31987 crotalus vi p31981 crotalus ba p31984 crotalus mo p31985 crotalus vi p31990 lachesis mu O93516 agkistrodon O7t1t3 bothrops c p31980 sistrurus c p31989 bothrops co p31980 crotalus at p31986 crotalus at p31986 crotalus vi O90222 agkistrodon

PF01421;

Reprolysin;

PR00289; DISINTEGRIN. PD000664; Disintegrin; SM00050; DISIN; 1.

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SMART; SM00050;
PROSITE; PS50215
PROSITE; PS00427
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SUBUNIT.
TISSUE=Venom gland;
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             "Molecular cloning and functional expression homedimeric disintegrin from southern copper Arch. Biochem. Biophys. 375:278-288(2001).
-i- FUNCTION: The metalloproteinase is a prob-
                                                                                                                                                                                              Viperidae; Crota
NCBI_TaxID=8713;
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iperidae; Crotalinae; Agkistrodon.
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PS50215; ADAM MEPRO; 1.

PS50427; DISINTEGRIN_1; 1.

; PS50214; DISINTEGRIN_2; 1.

; PS00142; ZINC_PROTEASE; 1.

; PS00142; ZINC_PROTEASE; 1.

requilation; Cell adhesion; Direct protein sequencing;

requilation; Cell adhesion; Direct protein sequencing;
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                                                                                                PubMed=10700384; DOI=10.1006/abbi.1999.1682; itter M.R., Swenson S.D., Argounova S., Epstein
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Pred. No. 5.4
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Spacer peptide (Potential).
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PROSITE; PS50215; ADAM MERRO; 1.

PROSITE; PS00427; DISINTEGRIN 1; 1.

PROSITE; PS50214; DISINTEGRIN 2; 1.

PROSITE; PS00142; ZINC PROTEASE; 1.

Blood coagulation; Cell adhesion; D
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IIb/beta-3, alpha-5/beta-1, alpha-V/beta-3, and alpha-V/beta-5.
blocks cancer cell adhesion to fibronectin and vitronectin and thus prevents invasion of cancer cells.
-!- COFACTOR: Binds 1 zinc ion per subunit.
-!- SUBCULIVIAR Homodimer; disulfide-linked (disintegrin).
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: Belongs to the peptidase M12B family.
-!- SIMILARITY: Contains 1 disintegrin domain.
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pfam; PF01562; Pep_M12B_propep;
Pfam; PF011621; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
PRODOM; PD000664; Disintegrin;
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InterPro; IPR006025; Pept M_Zn_BS.
InterPro; IPR001590; Peptidase_M12B.
InterPro; IPR002870; Peptidase_M12B_N.
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InterPro; IPR001762; Disintegrin.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR006025; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B N.
Pfam; PF001562; Pep M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
PROSITE; PS00215; ADDAM MEPRO; 1.
PROSITE; PS00215; ADDAM MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 1; FALSE NEG.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC PROTEASE; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AB078906; BAC55947.1; -. HSSP; P15167; 1DTH.
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J. Biochem. 130:407-415(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=12450389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: Expressed by the venom SIMILARITY: Belongs to the peptidase M12B: SIMILARITY: Contains 1 disintegrin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY:
SIMILARITY: Belongs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rich plasma.
COFACTOR: Binds 1 zinc
SUBUNIT: Piscivostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: The metalloproteinase is a probable venom zinc that acts in hemorrhage (By similarity).
FUNCTION: Piscivostatin inhibits fibrinogen interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      platelet receptors expressed on glycoprotein IIb-IIIa com
Acts by binding to the glycoprotein IIb-IIIa receptor on
platelet surface and inhibits both App-induced platelet
aggregation and platelet aggregate dissociation in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D., Morita T.
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Metal-binding;
1 20
21 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      piscivostat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOI=10.1021/bi0258768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         license agreement
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| heterodimer
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of Agkistrodon piscivorus
atin on platelet
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Matches 61
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05-JUL-2004
05-JUL-2004
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                                               ProDom; PD000664; Disintegrin; 1
SMART; SM00050; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN 1;
PROSITE; PS50214; DISINTEGRIN 2;
                                                                                                                Pfam; PF00200; Disintegrin; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
PRINTS; PR00680; PTREFOIL.
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SEQUENCE FROM N.A.
Chung K.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Platelet aggregation Name=salmosin;
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METAL
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                                                                                                                                                                                                                                Kang I.C., Chung K.H., Lee S.J., Yun "Purification and molecular cloning o inhibitor from the snake (Agkistrodon Thromb. Res. 0:0-0(1998).

EMBL; AF054626; AAC08997.1; -.

EOG; GO:0007229; P:integrin-mediated s
                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
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Viperidae; Crotalinae; (
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                                                                                                                                                                                IPR001762; Disintegrin.
IPR001590; Peptidase_M12B
IPR000519; P_trefoil.
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 11407 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
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el. 27, Last sequence update)
el. 27, Last annotation updat
inhibitor disintegrin (Fragm
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93.8%;
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No. 4.7e-31;
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n halys brevicaudu
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(Fragment)
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RESULT
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Matches 56
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF367868; AAK73517.1; -.

R PIR; A59409; A59409.

R PDB; 113x; NMR; A=245-317.

R GO; GO:0004222; F:metalloendopeptidase activity; IEA.

R GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

R GO; GO:0006509; Disintegrin; 1.

R Pfam; PF00200; Disintegrin; 1.

R Pfam; PF00200; Disintegrin; 1.

R Pfam; PF00200; Disintegrin; 1.

R PF1NTS; PR00289; DISINTEGRIN.

R PFNINTS; PR00289; DISINTEGRIN.

R PFODOm; PD000664; Disintegrin; 1.
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Best Local Similarity
Matches 56; Conserv
           Q9DGH6 PRELIMINARY;
Q9DGH6;
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-MAR-2004 (TrEMBLrel. 2
Saxatilin (Fragment).
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                             PROSITE; P850215; ADAM_MEPRO; 1.
PROSITE; P850427; DISINTEGRIN 1; 1.
PROSITE; P850214; DISINTEGRIN 2; 1.
PROSITE; P800142; ZINC_PROTEASE; UNKNOWN_1.
NON_TER 1 1
SEQUENCE 317 AA; 35109 MW; 9851177BCBE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euterebr
Lenidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
TISSUE=Venom gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agkistrodon halys brevicaudus (Korean slamosa snake) (Gloydius halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=hxl-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q90WC0
                                                                                                                                                                                                                                                                                                                                                     SMART; SM00050; DISIN; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=259325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /iperidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      orevicaudus)
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                                                                                                                                    314 PFHA 317
                                                                                                                                                                                   254
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                                                                                                                                                                                               APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
                                                                                                                                                                                   SPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDYCNGISAGCPRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPGNPCCDAATCKLRQGAQCAEGLCCDQCRFMKEGTICRRARGDDLDDYCNGISAGCPRN
                                                                                                                                                           PFHA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crotalinae; Gloydius
 halys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
pallas
                                                                                                                                                                                                                                          90.6%;
87.5%;
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19, Last
26, Last
                      16,
26,
 (Chinese
                      Created)
Last seq
Last ann
                                                                                                                                                                                                                               Score 346; DB
Pred. No. 2.8e
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last annotation update)
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Pred.
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                                                                                                                                                                                                                                                                                9851177BCBE2202E CRC64;
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                      sequence update) annotation updat
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No. 1.1e-29;
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                                                                       73
 mocassin) (Gloydius
                                                                                                                                                                                                                               DB 2; I
2.8e-29;
nes 3;
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                       update)
                                                                                                                                                                                                                                                        Length 317;
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RESULT 7
Q90221
ID Q902
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Best Local S
Matches 56
Query Match
                                                                                                                                                                                                                                                                                                                                                    "Halystatin, a novel disintegrin from agkistrodon halys, inhibitor of bone resorption and platelet aggregation."; Takeda Kenkyusho Ho 53:39-56(1994). EMBL; D28871; BAA06027.1; -. HSSP; P21859; 1J2L.
                                           SMART; SM00050; DISIN; 1
PROSITE; PS50215; ADAM P
PROSITE; PS00427; DISINT
PROSITE; PS00427; DISINT
PROSITE; PS50214; DISINT
NON_TER
1
SEQUENCE 117 AA; 1268
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Q90221;
Q10221;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Q1-OCT-2003 (TremBLrel. 25, Last annotation update)
Q2-Prepro-halystatin 2 (Fragment).
Q3-Prepro-halystatin 2 (Fragment).
Q3-Prepro-halystatin 2 (Fragment).
Q4-Prepro-halystatin 2 (Fragment).
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PROSITE; PS50214; DISINTEGRIN 2; 1.
NON_TER 1 1
                                                                                                                                                                                            Pfam; PF00200; Disintegrin; 1. Ffam; PF01421; Reprolysin; 1. PRINTS; PR00289; DISINTEGRIN. ProDom; PD000664; Disintegrin;
                                                                                                                                                                                                                                                                                             MEROPS; M12.134; -.
GO; GO:0004222; F:metalloendopeptidase activity; TEA
GO; GO:0006508; P:proteolysis and peptidolysis; TEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam, PF00200; Disintegrin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Venom gland;
TISSUE=Venom gland;
Koh Y.-S., Hong
to the !
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
NCBI_TaxID=8714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lepidosauria; Squamata; Sclerogl
Viperidae; Crotalinae; Gloydius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
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                                                                                       PS50215; ADAM_MEPRO; 1.
PS00427; DISINTEGRIN_1;
PS50214; DISINTEGRIN_2;
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larity 87.5%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
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                                                12686 MW;
90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 345; DB
Pred. No. 1e-2
5; Mismatches
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EMBL/GenBank/DDBJ
Score 345;
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DB
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Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                             Query Match
Best Local S
Matches 56
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EMBL; AF051789; AAD02654.1; -.

RISSP; P21859; JUZL.

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0005840; C:ribosome; IEA.

GO; GO:0004222; F:metalloendopeptidase activity; IEA.

GO; GO:0004735; F:structural constituent of ribosome; IEG.

GO; GO:0006412; P:protein biosynthesis; IEA.

GO; GO:0006589; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001762; Disintegrin.

InterPro; IPR001590; Peptidase M12B.

InterPro; IPR001890; Peptidase M12B.

InterPro; IPR002870; Peptidase M12B.

InterPro; IPR001815; Ribosomal L32E.

InterPro; IPR001515; Ribosomal L32E.
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                                                                                                                                                              Pfam; PF01562; Pep M12B propep; 1.
Pfam; PF01421; Reprolysin; 1.
Pfam; PF01421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; pD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PR0SITE; PS50215; ADAM MEPRO; 1.
PROSITE; PS50214; DISINTEGRIN 1; 1.
PROSITE; PS00427; DISINTEGRIN 2; 1.
PROSITE; PS00442; ZINC_PROTEASE; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jeon O.H., Kim D.S.;
"Molecular cloning and functional characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=brevicaudus; TISSUE=Venom; MEDLINE=99337693; PubMed=10406963.
                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                               Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                metalloprotease."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8714;
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Viperidae; Crotalinae; Gloydius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pallas)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Mt-d;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metalloprotease.
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                                             419
 479
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                      62
                                                                                                                                                                                                                                                                            PF00200; Disintegrin; 1.
                                                                                                                                                         .oprotease;
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                                                                                                        Similarity
                                            PFHA
                      PFHA 65
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                                                                                                                                           482 AA;
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                                                                                             Conservative
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482
                                                                                                                                                         Protease.
                                                                                                                                           53409 MW;
                                                                                                    90.3%;
87.5%;
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13,
26,
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Last sequence update)
Last annotation updat
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                                                                                          Score 345; DB 2; Pred. No. 5.2e-29; S; Mismatches 3;
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5; Mismatches 3;
                                                                                                                                           C6014BBE87BC8B15 CRC64;
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                                                                                                                  Length 482;
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                                                                                           Gaps
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RESULT 9
073795
ID 073795
AC 073795;
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DR HSSP; P21859; 1J72L.

R GO; GO:0005622; C:intracellular; IEA.

R GO; GO:0004222; F:metalloendopeptidase activity; IE.

R GO; GO:0003735; F:structural constituent of ribosome; GO; GO:0006412; P:protein biosynthemia.
                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                     Matches
Q98SP2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequenc
01-MAR-2004 (TrEMBLrel. 26, Last annotat
Bothrops jararaca;
Bothrops jararaca; Chordata; Craniata;
Eukaryota; Metazoa; Chordata; Craniata;
Lepidosauria; Squamata; Scleroglossa; Seviperidae; Crotalinae; Bothrops.
NCBI_TaxID=8724;
                                                                                                                                                                                                                                                                                                                             PROSITE; PS50215; ADAM_MEPRO; 1.
PROSITE; PS00427; DISINTEGRIN 1; 1.
PROSITE; PS50214; DISINTEGRIN 2; 1.
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
Metalloprotease; Protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001515; Ribosomal L32E.
                                                                                                                 Q98SP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lepidosauria; Squamata; Sclerogl
Viperidae; Crotalinae; Gloydius.
NCBI_TaxID=8714;
                                                                                                                                                                                                                                                                                                                                                                                                              Pfam, PF00200; Disintegrin; 1.
Pfam, PF01.562; Pep M12B propep; 1.
Pfam, PF01.421; Reprolysin; 1.
PRINTS; PR00289; DISINTEGRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Agkistrodon halys pallas pallas).
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01-MAR-2004
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                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=brevicaudus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metalloprotease.
                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000664; Disintegrin; 1.
                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO:0006508; P:proteolysis and peptidolysis; IEA
                                                                                                                                                                           502
                                                                                                                                                                                                                        442
                                                                                                                                                                                                62 PFHA 65
                                                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                        SM00050; DISIN; 1
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                    505 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (TrEMBLrel.
) (TrEMBLrel.
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                    56336 MW;
                                                                                                                                                                                                                                                                               89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Chinese water
                                                                                                                                                                                                                                                                     <u>ت</u>
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                Score 342; DB 2;
Pred. No. 1.1e-28;
                         Craniata; Vertebrata; Euteleostomi;
oglossa; Serpentes; Colubroidea;
                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                    C96E99FC9C05378F CRC64;
                                                                                                                                                                                                                                                                      Mismatches
                                                                    sequence update) annotation update)
                                                                                                                   477
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                        Serpentes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mocassin) (Gloydius halys
                                                                                                                   A
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                                                                                                                                                                                                                                                                                           Length 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IEA.
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RESULT
Q7SZD5
A CONTRACTOR OF THE CONTRACTOR
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Best Local S
Matches 55
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InterPro; IPR001500; Peptidase M12B.
InterPro; IPR001500; Peptidase M12B.
InterPro; IPR008025; Pept_M_Zn_BS.
InterPro; IPR001515; Ribosomal_L32E.
Pfam; PF00200; Disintegrin; 1.
Pfam; PF01562; Pep_M12B_propep; 1.
Pfam; PF01162; Rep_M12B_propep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q7SZD5
Q7SZD5;
Q1-QCT-2003 (
Q1-QCT-2003 (
Q1-MAR-2004 (
                          Integrin.
                                                                                                                                                                                                         TISSUE-Snake venom gland;
Sun D.-J., Yang T.-S.;
Sun bill, Yang T.-S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ
EMBL; AY204249; AAP20644.1; -.
HSSP; P21859; 1JZL.
GO: 00007229; P:integrin-mediated signaling
InterPro; IPR001762; Disintegrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disintegrin (Fragment).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00289; DISINTEGRIN.

Prodom; PD000664; Disintegrin; 1.

SMART; SM00050; DISIN; 1.

PROSITE; PS00215; ADAM MEPRO; 1.

PROSITE; PS00427; DISINTEGRIN 1; 1.

PROSITE; PS00142; DISINTEGRIN 2; 1.

PROSITE; PS00142; DISINTEGRIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Silva C.A., Martins de Camargo A.C., de Toledo Serrano S
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF34531; AAK15542.1; -
GO; GO:0005432; C:intracellular; IEA.
GO; GO:0005404; C:ribosome; IEA.
GO; GO:0005404; C:ribosome; IEA.
GO; GO:0005404; F:metalloendopeptidase activity; IEA.
GO; GO:0006412; F:metalloendopeptidase activity; IEA.
GO; GO:0006412; F:protein biosynthesis; IEA.
GO; GO:0006412; F:protein biosynthesis; IEA.
GO; GO:0006412; F:protein biosynthesis; IEA.
SEQUENCE
                                                                          PRODOM; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
PROSITE; PS00427; DISINTEGRIN 1;
PROSITE; PS50214; DISINTEGRIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                          Pfam; PF00200; Disintegrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=35671;
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GO:0005840; C:ribosome; IEA.
GO:0004222; F:metalloendopeptidase activity; IEA.
GO:0004222; F:metalloendopeptidase activity; IEA.
GO:0003735; F:structural constituent of ribosome
GO:0006412; P:protein biosynthesis; IEA.
GO:0006508; P:proteolysis and peptidolysis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 PGNPCCDAVTCKLRPGAQCAEGLCCDQCRFMKEGTVCRRARGDDMDDYCNGISAGCPRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
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3 (TrEMBLrel. 25,
4 (TrEMBLrel. 26,
73
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$
7768
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87.3%;
MΨ;
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Last
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Pred. No. 1.8e-28;
4; Mismatches 4
615509DF966882EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence update) annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    474
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RESULT 13
Q801Z4
ID Q801Z4
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Q7SZD9
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Best Local S
Matches 55
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InterPro; IPR001890; Peptidase_M12B.
InterPro; IPR0018970; Peptidase_M12B.
InterPro; IPR006025; Pept M Zn BS.
InterPro; IPR001815; Ribosomal_L32E.
InterPro; IPR001864; Disintegrin; 1.
InterPro; IPR001864; Disintegrin; 1.
InterPro; IPR0018664; Disintegrin; 1.
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Q7SZD9;
Q7SZD9;
01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 26, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Metalloproteinase/disintegrin ussurin.
Metalloproteinase (Korean viper) (Gloydius ussuriensis).
Agkistrodon caliginosus (Korean viper) (Gloydius ussuriensis).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P21859; 1/2L.

GO; GO:0005622; C:intracellular; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0004222; F:metalloendopeptidase activity; IEA.
GO; GO:000725; F:structural constituent of ribosome;
GO; GO:0007229; P:integrin-mediated signaling pathway;
GO; GO:0007229; P:integrin-mediated signaling pathway;
GO; GO:0006412; P:protein biosynthesis; IEA.
GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
                                                                                                                                                                                                                                                       Integrin.
SEQUENCE
                                                                                                                                                                                                                                                                              SMART; SM00050; DISIN; 1.

PROSITE; PSS0215; ADAM MEPRO; 1.

PROSITE; PS00427; DISINTEGRIN 1; 1.

PROSITE; PSS0214; DISINTEGRIN 2; 1.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Snake venom gland;
Sun D.-J., Yang T.-S.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AY204245; AAP20640.1; HSSP; P21859; 1J2L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=35671;
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                                                                            474
                                                                                                                                    414
                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 DAPANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                             Similarity
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                                                                                                                                                   DAPANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NPFHA
                                                                                                                                    DSPGNPCCDAATCKLRPGAQCAEGLCCEQCRFMKEGTVCRIARGDDMDDYCNGISAGCPR
                                                                                                                                                                                                                                                        478
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                                                                                                                                                                                               Conservative
                                                                            478
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                                                                                                                                                                                                                                                        53443 MW;
                                                                                                                                                                                                           88.7%;
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                                                                                                                                                                                             6
                                                                                                                                                                                             Score 339; DB
Pred. No. 2.3e
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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Pred. No. 4.5e-29;
                                                                                                                                                                                                                                                        CD2FBC975F62A771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                               4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    databases
                                                                                                                                                                                                                                                        CRC64;
                                                                                                                                                                                                                         Length 478;
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PRELIMINARY;

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PRINTIPE PROPERTY OF THE PROPE
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Best Local S
Matches 55
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Q1-JUN-2003 (TrEMBLrel.:
Q1-JUN-2003 (TrEMBLrel.:
Q1-MAR-2004 (TrEMBLrel.:
Disintegrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRIJE
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05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Zinc metalloproteinase jerdonitin precursor (EC 3.4.24.-) [Contains Disintegrin jerdonitin].
Trimeresurus jerdonii (Jerdon's pit-viper) (Protobothrops jerdoni).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea;
Viperidae, Crotalinae, Trimeresurus.
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NON TER
SEQUENCE
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Pfam; PF00200; Disintegrin; 1.
PRINTS; PR00289; DISINTEGRIN.
ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>မ</u>
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Submitted (MAR-2003) to the EMBL,
EMBL; AY259516; AAO75107.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bothrops alternatus.
Eukaryota; Metazoa; Chordata; Craniata;
Lepidosauria; Squamata; Scleroglossa; Se
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22873278; Pu
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                                                                                                                                                                                                                                                                                     Biochem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=64174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14
comprises metalloproteinase and disintegrin domains.";
ochem. Blophys. Res. Commun. 310:182-187(2003).
- FUNCTION: The metalloproteinase is a probable venom zinc prote
that acts in hemorrhage (By similarity).
- FUNCTION: Jerdonitin inhibits fibrinogen interaction with plat
receptors expressed on glycoprotein IIb-IIIa complex. Acts by
binding to the glycoprotein IIb-IIIa receptor on the platelet
surface and inhibits aggregation induced by ADP, thrombin,
platelet-activating factor and collagen (By similarity).
- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
                                                                                                                                                                                                                                                                                                                                           new protein structure of P-II class snake venom metalloproteinases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P; P21859; 1J2L.
GO:0007229; P:integrin-mediated
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AA;
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, Wu J.-B., Zhou
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460-484.
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X.-D., Lu Q.-M., Wang
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Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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RESULT 15
DISG TRIAB STANDARD; PRT; 73 AA.

AC P62384; P17496;
PT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-JUL-2004 (Rel. 44, Last annotation update)
DI 05-JUL-2004 (Rel. 44, Last annotation update)
DE Disintegrin albolabris (Platelet aggregation activation inhibitor).
OS Trimeresurus albolabris (White-lipped pit viper).
OS Trimeresurus albolabris (White-lipped pit viper).
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Matches
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Pfam; PF0152; Pep_M12B_propep; 1.

Pfam; PF01421; Reprolysin; 1.

PRINTS; PR00289; DISINTEGRIN.

PRODOM; PD000664; Disintegrin; 1.

SMART; SM00050; DISIN; 1.

PROSITE; PS50215; ADAM_MEPRO; 1.

PROSITE; PS50214; DISINTEGRIN 1; 1.

PROSITE; PS50214; DISINTEGRIN 2; 1.

PROSITE; PS50214; DISINTEGRIN 2; 1.

PROSITE; PS50214; DISINTEGRIN 2; 1.
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ACT_SITE
METAL
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InterPro; IPR001762; Disintegrin.
InterPro; IPR001590; Peptidase M12B.
InterPro; IPR002870; Peptidase M12B_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom
-!- SIMILARITY: Belongs to the peptidase M12B f
-!- SIMILARITY: Contains 1 disintegrin domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Hydrolase; Metal-binding;
                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                            424
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90.2%;
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By similarity.
Zinc (catalytic) (Probab
Zinc (catalytic) (Probab
Zinc (catalytic) (Probab
Zinc (catalytic),
Potential.
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MEDILINE=97052455; PubMed=8897089;

Smith K.J., Jaseja M., Lu X., Williams J.A., Hyde E.I., T

Smith K.J., Jaseja M., Lu X., Williams J.A., Hyde E.I., T

"Three-dimensional structure of the RGD-containing snake
albolabrin in solution, based on 1H NMR spectroscopy and
annealing calculations.";
                                                                                                                                                                                                                                                                   SEQUENCE
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Jaseja M., Smith K.J., Lu X., Williams J.A., Trayer H., Trayer I.P.,
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activity.";
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Niewiarowski S.;
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Viperidae; Crotalinae; 7
NCBI_TaxID=8765;
[1]
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ProDom; PD000664; Disintegrin; 1.
SMART; SM00050; DISIN; 1.
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TISSUE=Venom;
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PROSITE; PS50214; DISINTEGRIN_2; 1.
Blood coagulation; Cell adhesion; D
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TISSUE SPECIFICITY: Expressed by the venom gland.
SIMILARITY: Belongs to the disintegrin family.
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FUNCTION: Inhibits fibrinogen interaction with platelet receptors expressed on glycoprotein IIb-IIIa complex. Acts by binding to the glycoprotein IIb-IIIa receptor on the platelet surface and inhibits aggregation induced by ADP, thrombin, platelet-activating factor and collagen.
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Pred. No. 1.5e-28;
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Probable.
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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US-07-623-611-8
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ALIGNMENTS

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PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA TITLE OF INVENTION: CONTORTROSTATIN (CN) AND TITLE OF INVENTION: OTHER CONDITIONS FILE REFERENCE: 1279-33863/09801388 CURRENT APPLICATION NUMBER: US/09/460,295B CURRENT FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Agkistrodon contortrix
FILING DATE:
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; APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
; ITILE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
;INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
;THOSE INHIBITORS AND COMPOSITIONS USING THEM
; NUMBER OF SEQUENCES: 22
; CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;SEQ ID NO:21:
; LENGTH: 72
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LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Patent No. 5182260
APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
APPLICATI: NOT SEQUENCES ENCODING SNAKE VENOM
;INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
;THOSE INHIBITORS AND COMPOSITIONS USING THEM
;NUMBER OF SEQUENCES: 22
;CURRENT APPLICATION DATA;
 Query Match
Best Local S
Matches 55
                                                                                    SEQ ID NO:2:
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Best Local
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                                                                                              PILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 303,585
PILING DATE: 27-JAN-1989
PILING DATE: 27-JAN-1989
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FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
                                                                      LENGTH: 73
                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
APPLICATION NUMBER: 303,590
FILING DATE: 27-JAN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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             88.2%;
87.3%;
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Score 337; DB 6; Length 73; Pred. No. 1.6e-26; 5; Mismatches 3; Indels
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RESULT 5
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US-07-965-674-14
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APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
APPLICATION NUMBER: 303,590
FILING DATE: 27-JAN-1989
SEQ ID NO:2:
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APPLICANT: MARAGANORE, JOHN M.;JAKUBOWSKI, JOSEPH A.
TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
ITHOSE INHIBITORS AND COMPOSITIONS USING THEM
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Knight, Linda C.
TITLE OF INVENTION: Thrombus
TITLE OF INVENTION: Radiolabe
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Knight
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM PS/2
                                                CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                   SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      ADDRESSEE: Temple University - Of The Common-
ADDRESSEE: wealth System of Higher Education
STREET: 406 University Services Building
CITY: Philadelphia
STRTE: Pennsylvania
                                                                                 APPLICATION NUMBER: US
FILING DATE: 19921019
                                                                                                                                                  OPERATING SYSTEM: MS-DOS
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FILING DATE: 01-NOV-1989
                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                     COUNTRY:
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les 55; Conserv
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87.3%;
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RESULT 8
US-09-243-640-13
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US-08-993-165-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Unger, Evan C
APPLICANT: Wu, Yunqiu
TITLE OF INVENTION: Optacoustic Contrast Agents And Methods For Their Use
FILE REFERENCE: UNGR1224
CURRENT APPLICATION NUMBER: US/08/993,165A
CURRENT FILING DATE: 1997-12-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08993165A Patent No. 6123923
                                                                                                            GENERAL INFORMATION:
                                                                                                                            Sequence 13, Application US/09243640 Patent No. 6521211
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Best Local Similarity
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Best Local :
             APPLICANT: Unger, Evan C
APPLICANT: Shen, Dekang
APPLICANT: Wu, Guanli
TITLE OF INVENTION: No. 6521211el Methods Of Imaging
TITLE OF INVENTION: Compositions
FILE REFERENCE: DUP-0463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: No. 5380646e INFORMATION FOR SEQ ID NO:
CURRENT APPLICATION NUMBER: US/09/243,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 60:
TELECOMMUNICATION INFORMATION:
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LENGTH: 73 amino acids
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TELEFAX: (215) 568-5549
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                                                                                                                                                                                                                                                      62 PFHA 65
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Pred. No. 3.2e-26;
5; Mismatches 5
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Pred. No. 3.2e-26;
5; Mismatches 5
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US-08-929-847-15
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LENGTH: 73
TYPE: PRT
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CURRENT FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 73
                                                                                                      Matches
                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08929847 Patent No. 6548047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                    APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Thermal Preactivation Of Gaseous Precursor Filled Compositions
FILE REFERENCE: BMS0441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE: OTHER INFORMATION: Description of Artificial Sequence: No.
                                                                                                                                                                     OTHER INFORMATION: Completely synthetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                   Local Similarity
                                                10 SPANPCCDAATCKLLPGAQCGEGLCCDQCSFMKKGTICRRARGDDLDDYCNGISAGCPRN
70
                        62 PFHA 65
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                                                                           2 APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN 61
PLHA
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84.4%;
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                                                                                                    Score 334; DB 4; L
Pred. No. 3.2e-26;
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Pred. No. 3.2e-26;
5; Mismatches 5
                                                                                                                              Length 73;
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RESULT 10
US-09-460-295B-9
; Sequence 9, Application US/09460295B
; Patent No. 6710030
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA

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APPLICANT: Unger, Evan C.
TITLE OF INVENTION: No. 6716412el Methods OF
TITLE OF INVENTION: Filled Compositions
FILE REFERENCE: UNGR1600
CURRENT APPLICATION NUMBER: US/09/813,484
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 08/929,847
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 73
TYPE: PRT
ORGANISM: Trimeresurus albolabris
US-09-460-295B-9
                                                                                                                         RESULT 12
PCT-US93-09523-14
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                                                 Sequence 14, Application PC/TUS9309523
GENERAL INFORMATION:
APPLICANT: Temple University - Of APPLICANT: System of Higher Education
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15, Applica Patent No. 6716412 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Completely synthetic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
   APPLICANT:
APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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T: Temple University - Of The T: System of Higher Education T: Knight, Linda C. and T: Maurer, Alan H. INVENTION: Thrombus Detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APANPCCDAATCKLTTGSQCADGLCCDQCKFMKEGTVCRRARGDDLDDYCNGISAGCPRN
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   Thrombus Detection
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Pred. No. 3.2e-26;
5; Mismatches 5;
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Pred. No. 3.2e-26;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: KIM, DOO-Sik

APPLICANT: CHUNG, KWANG HOE

APPLICANT: CHUNG, KWANG HOE

APPLICANT: KANG, In-Cheol

TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS JUST

CURRENT APPLICATION NUMBER: US/09/776,268A

CURRENT FILING DATE: 2002-02-02

PRIOR APPLICATION NUMBER: US 09/335,088

PRIOR FILING DATE: 1999-06-17

PRIOR APPLICATION NUMBER: KR 99-20579

PRIOR FILING DATE: 1999-06-04

PRIOR APPLICATION NUMBER: KR 98-23778

PRIOR FILING DATE: 1998-06-23

JUMBER OF SEQ ID NOS: 7

SOFTWARE: Patentin version 3.1

SEQ ID NO 1

LENGTH: 73
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US-09-776-268A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 965,674
FILING DATE: 19 October 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordDerfect 5.1
CURRENT APPLICATION DATA:
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TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Temple University - Of The ADDRESSEE: Commonwealth System of Higher Education STREET: 406 University Services Building CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 54; Conserv
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REGISTRATION NUMBER: 30,480
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Pred. No. 3.2e-26;
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APPLICANT: Unger, Evan C.

TITIE OF INVENTION: Charged Lipids and Uses For ITITE OF INVENTION: Charged Lipids and Uses For Fills Reference: UNGR1592

CURRENT APPLICATION NUMBER: US/10/046,801

CURRENT FILING DATE: 2002-05-13

PRIOR APPLICATION NUMBER: US/09/540,448

PRIOR FILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 1997-09-08

NUMBER OF SEQ ID NOS: 37

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 15

LENGTH: 73
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US-10-046-801-15
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: No. 6403056el Sequence
US-09-540-448-15
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US-09-540-448-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. PATENTION:
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Charged Lipids and Uses For The Same
TITLE OF INVENTION: Charged Lipids and Uses For The Same
TITLE OF INVENTION: UNGRIS92
THE DEFERENCE: UNGRIS92
                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/10046801 Patent No. 6808720 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: UNGR1592
CURRENT APPLICATION NUMBER: US/09/540,448
CURRENT FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 08/925,353
PRIOR FILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 15
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Matches 54; Conservative
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Best Local Similarity
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                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: No. 6808720el Sequence
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                                                                                    Matches
                                                                                          Query Match
Best Local Similarity
                                                    70 PLHA 73
                                      62 PFHA 65
                                                                                    53;
                                                                                    Conservative
                                                                                         86.18;
2005, 08:20:24
                                                                                         Score 329; DB 4; Length 73; Pred. No. 1e-25;
                                                                                    Mismatches
                                                                                    5
                                                                                    Indels
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                                                                                    Gaps
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Search completed: November Job time: 43 secs ω ,

BEST AVAILABLE COPY

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Minimum DB
Maximum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.
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seq length: 2000000000
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382
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_RUB_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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                                                                                          / cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US09E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US11A_PUB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep: *
/ cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep: *
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160.927 Million cell updates/sec
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Result No.	Score	% Query Match	% Query Match Length DB ID	BB	ID	Description
ъ	382	100.0	į	14	US-10-439-532-2	Sequence 2, Appli
N	382	100.0	483	16	US-10-712-584-2	Sequence 2, Appli
ω	346	90.6		17	US-10-089-473A-10	Sequence 10, Appl
4	345	90.3		17	US-10-089-473A-1	Sequence 1, Appli
υ	334	87.4		9	US-09-813-484-15	Sequence 15, Appl
σ,	334	87.4		14	US-10-439-532-9	Sequence 9, Appli
7	334	87.4		16	US-10-712-584-9	Sequence 9, Appli
8	332	86.9		9	US-09-776-268A-1	Sequence 1, Appli
9	329	86.1		14	US-10-046-801-15	Sequence 15, Appl
10	322	84.3		14	US-10-439-532-8	Sequence 8, Appli
11	322	84.3		16	US-10-712-584-8	Sequence 8, Appli

Sequence 1132,	-	Ŋ.	49	0	191	45	
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Sequence		<u>.</u>	571	\vdash	•	42	
Sequence		Ļ	571	\vdash	195.5	41	
Sequence	US-09-840-277-1	9	282	μ	197	40	
Sequence		μ.	606	N	199	39	
Sequence	US-10-439-532-	ب	606	Ñ	199	38	
Sequence		_	76		207.5	37	
Sequence		L	616	56.0	214	36	
Sequence		y 9	611	57.3	219	3 5	
Sequence 2	ď	ø	400	58.4	223	34	
Seguence	-584-	_	478	•	228	33	
Sequence		ب	478	•	228	32	
Sequence	-584-	بر	68	59.7	228	31	
Sequence	14 US-10-439-532-11	ب	68		228	30	
Sequence	14 US-10-046-801-16	ب	68	•	238.5	29	
Seguence 16	ď	9	68	62.4	238.5	28	
Sequence		_	70	•	241.5	27	
Sequence	US-10-046-801-		69	•	243	26	
Sequence	14 US-10-046-801-17		70	•	244	25	
Sequence 17	9 US-09-813-484-17		70	63.9	244	24	
Sequence	d		69	•	258	23	
Sequence			481	•	261	22	
Sequence	15 US-10-383-588A-2		463	•	261	21	
Seguence	15 US-10-383-588A-6		71		261	20	
Sequence 8	9 US-09-921-823-8	9	195	69.4	265	19	
Sequence 23	US-09-921-823-2		111	•	265	18	
Sequence			73	٠	266	17	
Sequence	US-10-439-532-		73	•	266	16	
Sequence	Sn		478	٠	286	15	
Sequence	-10-712-		71	84.2	321.5	14	
Sequence	US-10-439-		71		321.5	13	
Sequence	US-09-832-501-		71		321.5	12	

ALIGNMENTS

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US-10-439-532-2

Sequence 2, Application US/10439532

Sequence 2, Application US/0030186884A1

SEQUENCE INFORMATION:
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST.
TITLE OF INVENTION: CONTORTROSSTATIN (SN) AND METHODS FOR ITS USE IN PREVENTING METAST.
TITLE OF INVENTION: CONTORTROSSTATIN (SN) AND METHODS FOR ITS USE IN PREVENTING METAST.
TITLE OF INVENTION: CONTORTROSSTATIN (SN) AND METHODS FOR ITS USE IN PREVENTING METAST.
TITLE OF INVENTION: CONTORTROSSTATIN (SN) AND METHODS FOR ITS USE IN PREVENTING METAST.
TITLE OF INVENTION: CONTORTROSSTATING METHODS FOR ITS USE IN PREVENTING METAST.
TITLE OF INVENTION: CONTORTROSSTATING METAST.
TITLE OF 
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Matches
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hes 65; Conservative 0;
479 NPFHA 483
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                                                                                                 61 NPFHA 65
                                                                                                                                                                                                         Score 382; DB 14;
Pred. No. 6.1e-32;
); Mismatches 0;
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APPLICANT: RITTER MATCHES

APPLICANT: RITTER (CN) AND METHODS FOR ITS USE IN PREVENTING METAST

TITLE OF INVENTION: CONFORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST

TITLE OF INVENTION: OTHER CONDITIONS

FILE REFERENCE: 1279-338M3/09801388

FILE REFERENCE: 1279-338M3/09801388

CURRENT FILING DATE: 2003-11-12

PRIOR APPLICATION NUMBER: US/10/712,584

CURRENT FILING DATE: 2000-06-08

PRIOR APPLICATION NUMBER: US/08/14,321

PRIOR FILING DATE: 1993-10-22

PRIOR APPLICATION NUMBER: US/08/14,423

PRIOR APPLICATION NUMBER: US/08/540,423

PRIOR APPLICATION NUMBER: US/08/540,691

PRIOR APPLICATION NUMBER: US/08/63,691

PRIOR APPLICATION NUMBER: US/08/63,691

PRIOR APPLICATION NUMBER: US/08/63,691

PRIOR APPLICATION NUMBER: US/08/63,691

PRIOR APPLICATION NUMBER: US/08/63,047

PRIOR APPLICATION NUMBER: US/09/163,047

PRIOR APPLICATION NUMBER: US/09/163,047
                                                                       APPLICANT: SOHN, Young-Dong
APPLICANT: YOU, Weon-Kyoo
APPLICANT: JANG, Yang-Soo
APPLICANT: HIH, Chin-Kyu
TITLE OF INVENTION: FOR PREPARING THE SAME
FILE REFERENCE: 0136/0K432US0
CURRENT APPLICATION NUMBER: US/10/089,473A
CCURRENT FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 10
LENGTH: 72
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US-10-089-473A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application No. US20 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 483
TYPE: PRT
ORGANISM: Agkistrodon contortrix
:-10-712-584-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1999-12-10 NUMBER OF SEQ ID NOS: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1
                LENGTH: 73
TYPE: PRT
ORGANISM: Agkistrodon halys brevicaudus
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APPLICANT: Unger, Evan C.
TITLE OF INVENTION: No. 6716412el Methods Of
TITLE OF INVENTION: Filled Compositions
FILE REFERENCE: UNGR1600
CURRENT ELLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: US/99/813,484
CURRENT FILING DATE: 1997-09-15
PRIOR FILING DATE: 1997-09-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.1
SEQ ID NO 15
LENGTH: 73
TYPE: PRT
ORGANIEM: Artificial Sequence
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Sequence 15, Application US/09813484
Publication No. US20010031243A1
GENERAL INFORMATION:
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; OTHER INFORMATION: Completely synthetic sequence
US-09-813-484-15
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LENGTH: 73
TYPE: PRT
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APPLICANT: CHUNG, Kwang-Hc
APPLICANT: KIM, Doo-Sik
APPLICANT: KOH, You-Seok
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APPLICANT: HUH, Chin-Kyu
TITLE OF INVENTION: NOVEL PROTEIN DERIVED FROM AGKISTRODON SAXATILIS EMELIANOV AND
TITLE OF INVENTION: FOR PREPARING THE SAME
FILE REFERENCE: 0136/0K432US0
CURRENT APPLICATION NUMBER: US/10/089,473A
CURRENT FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Agkistrodon saxatilis emelianov
                                  FEATURE:
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YOU, Weon-Kyoo
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                                                                                                                                                                                                                                          6716412el Methods Of Ultrasound Treatment Using Gas Or Gaseou
lled Compositions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 345; DB 17;
Pred. No. 8.8e-29;
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RESULT 7
US-10-712-584-9
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US-10-439-532-9
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                                PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILLING DATE: 2000-06-08
PRIOR PELICATION NUMBER: US 08/141,321
PRIOR FILLING DATE: 1993-10-22
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR APPLICATION NUMBER: US 08/632,691
PRIOR APPLICATION NUMBER: US 08/632,691
PRIOR PILING DATE: 1996-04-15
PRIOR APPLICATION NUMBER: US 08/745,603
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                                                                                                                                                                                                    Sequence 9, Application US/10712584
Publication No. US20040132659A1
GENERRAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: Markland, Francis S.
APPLICANT: Ritter, Markland, Francis S.
APPLICANT: Ritter, Markland
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
CURRENT FILING DATE: 2003-11-12
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SOFTWARE: PatentIn versions SEQ ID NO 9
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Best Local S
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Best Local (
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CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
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ORGANISM: Trimeresurus albolabris
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FILING DATE: 1996-11-08
APPLICATION NUMBER: US 09/163,047
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84.4%;
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Pred. No. 1.3e-27;
5; Mismatches 5;
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Pred. No. 1.3e-27;
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US-10-046-801-15
Sequence 15, Application US/10046801
Publication No. US20030054027A1
GENERAL INFORMATION:
APPLICANT: Unger, Evan C.
TITLE OF INVENTION: Charged Lipids and Uses For The Same
FILE REFERENCE: UNGR1592
CURRENT APPLICATION NUMBER: US/10/046,801
CURRENT FILING DATE: 2002-05-13
PRIOR APPLICATION NUMBER: US/09/540,448
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; ORGANISM: Agkistrodon halys brevicaudus
US-09-776-268A-1
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NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 73
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Best Local
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APPLICANT: CHUNG, KWANG Hoe
APPLICANT: CHUNG, KWANG Hoe
APPLICANT: KANG, In-Cheol
TITLE OF INVENTION: ANTI-TUMOR AGENT COMPRISING SALMOSIN AS AN ACTIVE INGREDIENT
FILE REFERENCE: 0136/19733-US1
CURRENT FILING DATE: 2002-02-02
PRIOR APPLICATION NUMBER: US 09/376,268A
CURRENT FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 99-20579
PRIOR APPLICATION NUMBER: KR 99-23778
PRIOR APPLICATION NUMBER: KR 98-23778
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NUMBER OF SEQ ID NOS: 7
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Pred. No. 1.3e-27;
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Sequence 8, Application US/10712584
Publication No. US20040132659A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: Markland, Francis S.
APPLICANT: Ritter, Matthew
ITITLE OF INVENTION: CONTORTROSTATIN (CN) AND ME
ITITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
CURRENT FILING DATE: 2003-11-12
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US-10-439-532-8
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publication No. US20030186894A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338N2/09801388
FILE REFERENCE: 1279-338N2/09801388
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SEQ ID NO 15
LENGTH: 73
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Best Local Similarity
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Best Local
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PRIOR APPLICATION NUMBER: 08/925,353
PRIOR FILING DATE: 1997-09-08
NUMBER OF SEQ ID NOS: 37
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PRIOR FILING DATE: 2000-06-08
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CURRENT FILING DATE: 2003-05-16
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TYPE: PRT
ORGANISM: Artificial Sequence
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82.8%;
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Pred. No. 4.2e-27;
6; Mismatches 5;
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Pred. No. 1.4e-25;
5; Mismatches 6;
                                                                            AND METHODS FOR ITS USE IN PREVENTING METAS'
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US-09-832-501-37
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CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: 60/229,358
PRIOR FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR APPLICATION NUMBER: 60/256,931
PRIOR FILING DATE: 2000-12-21
PRIOR PPLICATION NUMBER: 60/199,384
PRIOR FILING DATE: 2000-04-25
NUMBER OF SEQ ID NOS: 37
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Matches
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Matches
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LENGTH: 552
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                                                                                                Query Match
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Turner, Andrew J.
APPLICANT: Sadeghi, Homa
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Albumin Fusion Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ballance, David J. APPLICANT: Sleep, Darrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1996-04-15
PRIOR APPLICATION NUMBER: US 08/745,603
PRIOR FILING DATE: 1996-11-08
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: US09/460,295
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1995-10-10
PRIOR APPLICATION NUMBER: US 08/632,691
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                                                                                                                                                                       LENGTH: 71
                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PF542
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                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US09/591,552 FILING DATE: 2000-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/141,321 FILING DATE: 1993-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  489 SPANPCCDAATCKLIPGAQCGEGLCCDQCSFIEEGTVCRIARGDDLDDYCNGRSAGCPRN
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62 PFHA
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                                                                                    Similarity
                                                                                                                                                                                                                        PatentIn Ver. 2.1
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85.7%;
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                                                                  Score 321.5; DB 10
Pred. No. 2.5e-26;
5; Mismatches 3;
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Pred. No. 1.4e-25;
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                                                                                                  DB 10;
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62 PFH 64

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69

PFH

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; ORGANISM: Agkistrodon piscivorus US-10-712-584-7
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                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 71
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Best Local Similarity
Matches 54; Conserv
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Publication No. US20030186884A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338NZ/09801388
FILE REFERENCE: 1279-338NZ/09801388
Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: UNIVERSITY OF SOUTHERN CALIFORNIA
APPLICANT: Markland, Francis S.
APPLICANT: Mitter, Matthew
TITLE OF INVENTION: CONTORTROSTATIN (CN) AND METHODS FOR ITS USE IN PREVENTING METAST
TITLE OF INVENTION: OTHER CONDITIONS
FILE REFERENCE: 1279-338N3/09801388
CURRENT APPLICATION NUMBER: US/10/712,584
CURRENT FILING DATE: 2003-11-12
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR APPLICATION NUMBER: US 08/141,321
PRIOR APPLICATION NUMBER: US 08/540,423
PRIOR FILING DATE: 1993-10-22
PRIOR FILING DATE: 1995-10-10
PRIOR FILING DATE: 1995-10-10
PRIOR FILING DATE: 1995-10-10
                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/745,603
PRIOR FILING DATE: 1996-11-08
PRIOR APPLICATION NUMBER: US 09/163,047
PRIOR FILING DATE: 1998-09-29
PRIOR FILING DATE: 1998-09-29
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CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: US09/591,552
PRIOR FILING DATE: 2000-06-08
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PRIOR FILING DATE: 1999-12-10
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84.2%; Score 321.5;
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Pred. No. 2.5e-26;
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DB 16; Length 71;
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Search completed: November Job time : 171 secs

2005, 08:23:19

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US-10-078-866-2
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                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10078866 Publication No. US20030096393A1 GENERAL INFORMATION:
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                                                                                                                                                                                                      SEQ ID NO 2
                                                                                                    Matches
                                                                                                                           Query Match
                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/078,866
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: 60/270,276
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 8
SOFTMARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                      APPLICANT: FOX, BRIAN A APPLICANT: SHEPPARD, PAUL O.
                                                                                                                                                                                                                                                                                               FILE REFERENCE: 01-05
                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Disintegrin Homolog, zsnkl6
                                                                                                                                                             LENGTH: 478
TYPE: PRT
ORGANISM: Sistrurus miliarius
                                                                                                                Local
                                                 475 RFHA 478
                                                                                                   47;
                         62 PFHA 65
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                                                                 Similarity
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                                                                                                   Score 286; DB 14;
Pred. No. 7.3e-22;
8; Mismatches 9;
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                                                                                                                            Length 478;
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BEST AVAILABLE COPY

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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